

0420/0590

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## RAW SEQUENCE LISTING

DATE: 06/14/2001

PATENT APPLICATION: US/09/871,388

TIME: 10:25:52

Input Set : N:\Crf3\RULE60\09871388.txt  
 Output Set: N:\CRF3\06142001\I871388.raw

## SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:  
 4 (i) APPLICANT: Rubin, Gerald M.  
 5 Pan, Duoia  
 6 Rooke, Jenny  
 7 Yavari, Reza  
 8 Xu, Tian  
 9 (ii) TITLE OF INVENTION: KUZ: A Novel Family of Metalloproteases  
 10 (iii) NUMBER OF SEQUENCES: 10  
 11 (iv) CORRESPONDENCE ADDRESS:  
 12 (A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP  
 13 (B) STREET: 268 BUSH STREET, SUITE 3200  
 14 (C) CITY: SAN FRANCISCO  
 15 (D) STATE: CALIFORNIA  
 16 (E) COUNTRY: USA  
 17 (F) ZIP: 94104  
 18 (v) COMPUTER READABLE FORM:  
 19 (A) MEDIUM TYPE: Floppy disk  
 20 (B) COMPUTER: IBM PC compatible  
 21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
 22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
 24 (vi) CURRENT APPLICATION DATA:  
 C--> 25 (A) APPLICATION NUMBER: US/09/871,388  
 C--> 26 (B) FILING DATE: 31-May-2001  
 27 (C) CLASSIFICATION:  
 29 (vii) PRIOR APPLICATION DATA:  
 30 (A) APPLICATION NUMBER: 08/937,931  
 31 (B) FILING DATE:  
 33 (viii) ATTORNEY/AGENT INFORMATION:  
 34 (A) NAME: OSMAN, RICHARD A  
 35 (B) REGISTRATION NUMBER: 36,627  
 36 (C) REFERENCE/DOCKET NUMBER: B97-081  
 37 (ix) TELECOMMUNICATION INFORMATION:  
 38 (A) TELEPHONE: (415) 343-4341  
 39 (B) TELEFAX: (415) 343-4342  
 41 (2) INFORMATION FOR SEQ ID NO: 1:  
 42 (i) SEQUENCE CHARACTERISTICS:  
 43 (A) LENGTH: 5630 base pairs  
 44 (B) TYPE: nucleic acid  
 45 (C) STRANDEDNESS: double  
 46 (D) TOPOLOGY: linear  
 47 (ii) MOLECULE TYPE: cDNA  
 48 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 49 GTTTAAAAA AACCACCAAG CGAGTTGGAC GCGTAACTCT TTGTAACGGA TCTCGGAACG 60  
 50 CCGTGGGAGT CGGAAAATCG CTGGACGCGT GTTCGTGCGT TTGCATGTGT GCGTGCGTTC 120  
 51 GTGTGTGTGT GTGTGCTAAT GTGCGAGCGG GTGAGCGAAT AAAAATAAAT ATATATCGTC 180  
 52 AAGTCAGGCT TAAGAAATGT GCGCTAATCA AAGAAAATGC CCCCAATTCT GGCCAATTGA 240

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53	GAATTGTGGC	TAAACAAAAA	ATTCGACCGG	AGTTCAAAAA	TAAACAATCC	AGTGAATAAA	300
54	CACACAAAAT	CAATCAAAAA	AGAAGATTTT	TCTTTTAT	TTTCGCTTTT	AATTTATTAA	360
55	CGAGAATAAT	AAATAAATAA	ATAAATAAAT	ATAAACAAAA	ATAAAAATAT	AAGAAAAGTG	420
56	TACGTGACAA	GAGCTCGAAA	AGAAGTTGCA	ACAAATAGCA	AAAATAATTC	GTGCGTGCGA	480
57	AAAAGTGCTG	CGAAGTTTTA	TGGCCCATGC	AAAAAGTGCT	AAATTTGTAA	ATGGCATGGA	540
58	AAGTGCAAAG	CTCTGATTAA	AAAACCCGCG	AAGATTGGAG	TGCGAGGTGC	CGCCCAATAA	600
59	CGCAACCAAC	TACTGCCACA	AGGAAATTAT	TAAGACCAAT	CAACGACCAA	AAAAATAAAA	660
60	AATAAAACAA	AAGCAAGCAG	AAATTTGGTG	CTAGTTCTGT	TTAGTCGACA	GCCATCCACG	720
61	TTGGATCCCC	ATCGCAAATA	ATGTCATCAA	AATGTGCTTT	CAACATTGTA	TTCGTATCGA	780
62	TCATTTTCAT	CATCATCGTA	AATGGTTACG	CAAAAGATAT	TTCTGGAGTT	AAAAGAGGTC	840
63	ATGAACGACT	TAACGAATAC	ATATCCCACT	ATGAAACACT	CAACTATGAT	CACGAGCACA	900
64	TCCGAGCTAG	TCACAATAGA	GCGCGACGAT	CAGTGACCAA	AGATCAATAT	GTACATTTAA	960
65	AGTTTGCATC	ACATGGAAGA	GACTTCCATC	TTAGATTAAA	ACGTGATTTA	AATACATTTA	1020
66	GCAATAAGTT	AGACTTTTAT	GATAGCAAAG	GTCCCATTTG	TGTCTCCACG	GATCATATCT	1080
67	ATGAGGGCGA	AGTGATAGGG	GATCGTAATA	GTTATGTATT	TGGTTCCATA	CACAATGGGG	1140
68	TATTCGAGGG	TAAAATTATA	ACGGAACGTG	ATGCCTATTA	TGTTGAACAT	GCCAAACATT	1200
69	ATTTTCCAC	AAATCGCACG	GCGACAACAA	CACCACCATC	GACTTCGACG	ACATCCTCAG	1260
70	CAACAACAGT	CACAAAAAGC	ACACAACCAA	CACGGCCTTT	GGCCAAAAGC	AACACCAGTA	1320
71	CTACTGCCGT	TAATAGTAAG	ACAGAAAAC	TTATAAAGAA	AATTGCTGAA	TCCACAACGA	1380
72	CGAGCCAGCA	GCTTCCAGAA	TATACCGAAT	CGTCGTCGTC	GTCGTCGACA	ACAACATTCC	1440
73	CACCCACAAC	AGAGTATTTT	GAGGACGAAA	AGGAGCGTAA	TGCCGAGGAC	GAAGTTGATT	1500
74	TTCATCCCAT	TATCTACAAG	GAGTCACATG	TCGAGGACGC	CTACGAAAAT	GTGCGCGAAG	1560
75	GTCACGTGGC	CGGCTGTGGC	ATCACGGATG	AGGTCTCTCA	GTGGATGGAG	AACATACAAA	1620
76	ATTCAGCCGT	CGAAGAGTTG	CCGGAGCCCA	TGTCAAAGGA	CTATCAAAAG	CTCCACCGGA	1680
77	AGCAGCTGCA	CAAAAAGTCC	GCCCCACAGC	AACAACAGCA	GCCCCATCCG	CCGAAGAAGT	1740
78	ACATCAGCGG	GGATGAGGAC	TTCAAGTATC	CCCACCAGAA	GTACACGAAG	GAAGCTAACT	1800
79	TCGCCGAGGG	TGCATTCTAC	GATCCATCGA	CCGGACGTCG	CCTGGGCTCA	TCCGCCAACG	1860
80	TGGCCGACTG	GCATCAGCTC	GTCCACGAGC	GCGTCCGCCG	CGCCACCGAC	AATGGTGCTG	1920
81	GGGATAGGGG	CTCATCCGGT	GGATCTGGAC	GCGGTCGCGA	GGACAACAAG	AATACCTGCT	1980
82	CGCTCTACAT	TCAAACGGAT	CCATTGATAT	GGCGCCACAT	ACGCGAAGGC	ATTGCTGACC	2040
83	ACGATCGTGG	ACGCAAGTAC	GAGGTGGATG	AGAAAACGCG	CGAGGAAATC	ACATCGTTGA	2100
84	TTGCACATCA	CGTGACGGCC	GTTAATTACA	TTTACCGCAA	CACAAAGTTC	GACGGACGCA	2160
85	CCGAGCATCG	CAACATACGC	TTTGAGGTGC	AACGCATTAA	GATCGATGAC	GATTGCGCCT	2220
86	GTGCAATTC	CTACAATGGT	CCACACAATG	CCTTTTGCAA	TGAACACATG	GATGTCTCGA	2280
87	ACTTTTGTAA	TCTGCATTCC	CTAGAAGATC	ACTCGGACTT	TTGTTTGGCT	TACGTGTTCA	2340
88	CCTACAGAGA	TTTCACTGGC	GGCACTTTGG	GTCTGGCCTG	GGTGGCCAGT	GCGTCGGGAG	2400
89	CCTCTGGTGG	AATTGCGGAG	AAGTACAAGA	CGTACACGGA	AACGGTGGGT	GGACAGTACC	2460
90	AGAGCACCAA	GCGATCACTC	AACACGGGCA	TCATCACCTT	TGTCAACTAC	AACAGTCGGG	2520
91	TGCCGCCGAA	AGTGTGCGAG	CTTACGTTGG	CACACGAGAT	TGGCCACAAC	TTTGGATCAC	2580
92	CTCACGATTA	CCCTCAGGAA	TGTCGTCCTG	GTGGCCTAAA	TGGCAATTAC	ATTATGTTCT	2640
93	CCAGTGCCAC	CTCCGGTGAT	AGGCCAAATA	ACTCCAAGTT	CTCGCCCTGC	TCCATTCCGA	2700
94	ACATCTCCAA	TGTCCTTGAC	GTGCTGGTGG	GCAACACGAA	GCGCGACTGC	TTCAAGGCCT	2760
95	CGGAAGGTGC	CTTCTGCGGC	AACAAGATCG	TGGAGTCTGG	CGAGGAATGC	GACTGTGGCT	2820
96	TCAACGAGGA	GGAGTGCAAG	GACAAGTGCT	GCTACCCGCG	TCTGATCAGC	GAGTACGACC	2880
97	AGTCGCTGAA	CTCCAGTGCC	AAGGGATGCA	CGCGCCGCGC	CAAGACCCAG	TGCTACCCAT	2940
98	CGCAGGGTCC	GTGCTGTCTG	TCCAATCCTT	GCACCTTTGT	GCCGACGAGC	TACCACCAGA	3000
99	AGTGCAAGGA	GGAGACGGAG	TGCAGCTGGT	CGAGCACATG	CAACGGAACC	ACGGCCGAGT	3060
100	GTCCCGAGCC	ACGTCATCGC	GATGACAAGA	CCATGTGCAA	CAATGGAACA	GCGCTATGCA	3120
101	TCCGCGGTGA	ATGTAGTGGA	TCGCCATGTT	TGCTCTGGAA	TATGACAAAG	TGCTTCCTTA	3180

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102	CCTCGACCAC	ACTGCCGCAC	GTGAGCAAGC	GCAAGTTGTG	CGACTTGGCC	TGCCAGGATG	3240
103	GCAATGACAC	CTCCACCTGC	CGCAGCACCA	GCGAGTTTGC	CGATAAATAT	AATATTCAAA	3300
104	AGGGTGGTAT	TAGTCTGCAG	CCCGGTTTCG	CATGCGATAA	TTTCCAGGGC	TACTGCGATG	3360
105	TGTTCCCTAA	GTGTCTGAGC	GTGGATGCCG	ATGGTCCGCT	TCTTCGGCTG	AAGAATTTGT	3420
106	TGCTCAACCG	GAAGACCCTG	CAAACGGTGG	CCGAGTGGAT	CGTCGACAA	TGGTACCTAG	3480
107	TGGTTCTGAT	GGGAGTGGCC	TTTATTGTGG	TCATGGGTTT	GTTTCATCAA	TGTTGTGCCG	3540
108	TGCACACGCC	CAGTTCCAAT	CCGAAGAAGC	GACGAGCTCG	TCGAATCAGC	GAAACTCTAA	3600
109	GAGCACCCAT	GAACACGTTG	CGTAGAATGC	AACGTCATCC	CAATCAGCGA	GGAGCAGGTC	3660
110	CTCGAAGCAT	CCCACCGCCG	GCACATGAGG	CGCAGCATT	TTCACGCGGC	GGAGATGGTC	3720
111	GCGGCGGCGG	CGGTGGAGGC	GGAGGTCGCC	ACGGTGGCTC	TAGGTCACAC	CATCAACAGC	3780
112	ATCCGCACGA	TTGGGATCGT	CATCAGGGTG	GCCACTCAAT	CGTCCCATTG	CCCACCGGCG	3840
113	GCAGCCATTC	AAGTCGCAAC	TCGGCGGCGA	ATCAAGCGAG	AAGAAGCGAT	GGACGAGGTC	3900
114	CACGATCCAC	CAGCAGTGGG	CGGCCGCGAG	CTATAGCCAG	CGGAAGCGGT	GCCGCGAGCG	3960
115	GAGCAGCGCG	ATCTCATGGC	GGGTACGGAG	CCGAACAGGC	GATACCGGGT	TCCATTGGTG	4020
116	GTGGTGTCCA	GGCGGCCATT	AGCAGCGGGC	GTGTGGTGGC	TCGGGCCCAG	CTGCCGCTGC	4080
117	CATTGCCGCC	GCCAAATGGA	CAGCAGCAAA	TGCAACAGCA	ACAACAACG	CAACTACAGC	4140
118	AACCGGCAAT	TTCGCCGCAG	CAGCAGCCGC	AGCAAGCGTT	CTACACGCCG	AAAGAACTAC	4200
119	CACCACGCAA	TAAGTCCCGA	TCATCACGTA	CCAACAACAC	CTCCAACACC	ACAACCACCA	4260
120	CCAACATCAT	CACAGCGGCA	GCCGGCAGTG	GGTCGGTCTC	GGGACCGGGC	TCGGGGGCGG	4320
121	GCAGTAGTAG	TAAGAGCAAG	AGCGGTAAAA	GTGCCAAAGC	CAAAGACTCA	AAGTCGCAAA	4380
122	AATCGCAGCA	GGCCAACAAC	AGTCGCAGCA	GCAGCAAGGA	GAAGGGCGTC	AAGCCAGTGC	4440
123	GCCGAAATAT	CGTTTATTAG	GAGCGGAACC	ATCACATTGC	CATACACAAC	ACTGAACGAA	4500
124	ATATAGCCCC	GAACCCAAAA	TATCAAATGC	AACCACATAT	AGAATCGCCC	GCTGCTAGTC	4560
125	ATCGAACTAC	ATGTATGAGT	TGTTGCTTCC	CATCCACCGA	CAAACACAAA	CAGAAAAGAA	4620
126	ATTATAATGA	TATTTTATTT	AATCGATGCA	ATTGGCGTCG	CGCCGCCTCC	GCTACAAGTA	4680
127	AGCTTTAGTC	GGCCGACATC	GTTGCACGAG	CAACAGCAGC	AGCAACATCA	TCTGCAGCAG	4740
128	CAGCAGCAGC	ATCAGCAGCA	ACTGGAGCCG	CAGCAGCAAC	ACGCCTATGC	CGATGCTTAT	4800
129	GCGGCCTTGG	GGCGGGGCCA	GTATGAGTCC	ACCACGCGGG	CGCCCAACAA	CAGCAAGGTT	4860
130	TGACAGCCAA	AAGTAGCAAT	GGAGCGCCAC	AAAAGGCCAA	AGGCTAAGCG	ACTCAAGCAG	4920
131	CAGAAGGAGC	CGCATACACA	GCAAACAACA	ACACAGCAAC	AAAAGCAAAA	ACAACATAAA	4980
132	TCAAATGAAC	TCAAATTTAA	TGTAAATGTA	ATTTTATATG	TAATTATTTT	TATTTAAACA	5040
133	GTGTTTGTAT	GCCACAAGGG	AAAACAGCCA	GCAACAAAAA	GAAAAATACA	AAAATAACAC	5100
134	AAAAAAGGAG	ACAAATTTTC	TAATACAGAA	AAAGCTGAAA	GTGAATGATA	TTTTTGATTA	5160
135	ACTAAATTAA	AATGAAAATA	CGAATGCAAA	TTATGAATAA	TAAAAGTAAT	TAAAAACGAC	5220
136	AACATGCATA	ATACATATAA	AGTTGCAAGT	TGCATATATA	TACATTTGTA	TGTATATATT	5280
137	TATTATGGAT	ACACAATTAT	TAAATAGCAG	CAGCCACAAC	AAACAAGTAA	TATACATGAA	5340
138	GAAAAACTAA	GGTTTAATTG	TATGAGAAAG	CATTCTATAT	GTCGGTGAGA	TTTCTAAGCG	5400
139	CTAGGCCGAA	ATACAAAATT	AATTACACAC	TTGAATAACA	AAATGTGTTT	TGTACAAAAA	5460
140	AAAAAAATG	AAATAAACAA	AAACAGTGCG	AATTAATTAA	GCGTCATTAT	AAAAAAAAGA	5520
141	ACGGAAACAA	CAAAGCATTT	AAATTGTATT	TATCTGTACC	GAAGCTAAAC	GTTTATTTAA	5580
142	AGCCGTCAAA	ATTGCATTTG	TAAACTAGCA	AAACAAAAAA	AAAAAAAAC		5630
144	(2) INFORMATION FOR SEQ ID NO: 2:						
145	(i) SEQUENCE CHARACTERISTICS:						
146	(A) LENGTH: 1239 amino acids						
147	(B) TYPE: amino acid						
148	(C) STRANDEDNESS: single						
149	(D) TOPOLOGY: linear						
150	(ii) MOLECULE TYPE: peptide						
151	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:						

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152 Met Ser Ser Lys Cys Ala Phe Asn Ile Val Phe Val Ser Ile Ile Phe
153 1 5 10 15
154 Ile Ile Ile Val Asn Gly Tyr Ala Lys Asp Ile Ser Gly Val Lys Arg
155 20 25 30
156 Gly His Glu Arg Leu Asn Glu Tyr Ile Ser His Tyr Glu Thr Leu Asn
157 35 40 45
158 Tyr Asp His Glu His Ile Arg Ala Ser His Asn Arg Ala Arg Arg Ser
159 50 55 60
160 Val Thr Lys Asp Gln Tyr Val His Leu Lys Phe Ala Ser His Gly Arg
161 65 70 75 80
162 Asp Phe His Leu Arg Leu Lys Arg Asp Leu Asn Thr Phe Ser Asn Lys
163 85 90 95
164 Leu Asp Phe Tyr Asp Ser Lys Gly Pro Ile Asp Val Ser Thr Asp His
165 100 105 110
166 Ile Tyr Glu Gly Glu Val Ile Gly Asp Arg Asn Ser Tyr Val Phe Gly
167 115 120 125
168 Ser Ile His Asn Gly Val Phe Glu Gly Lys Ile Ile Thr Glu Arg Asp
169 130 135 140
170 Ala Tyr Tyr Val Glu His Ala Lys His Tyr Phe Pro Thr Asn Arg Thr
171 145 150 155 160
172 Ala Thr Thr Thr Pro Pro Ser Thr Ser Thr Thr Ser Ser Ala Thr Thr
173 165 170 175
174 Val Thr Lys Ser Thr Gln Pro Thr Arg Pro Leu Ala Lys Ser Asn Thr
175 180 185 190
176 Ser Thr Thr Ala Val Asn Ser Lys Thr Glu Asn Phe Ile Lys Lys Ile
177 195 200 205
178 Ala Glu Ser Thr Thr Thr Ser Gln Gln Leu Pro Glu Tyr Thr Glu Ser
179 210 215 220
180 Ser Ser Ser Ser Ser Thr Thr Phe Pro Pro Thr Thr Glu Tyr Phe
181 225 230 235 240
182 Glu Asp Glu Lys Glu Arg Asn Ala Glu Asp Glu Leu Asp Phe His Ser
183 245 250 255
184 Ile Ile Tyr Lys Glu Ser His Val Glu Asp Ala Tyr Glu Asn Val Arg
185 260 265 270
186 Glu Gly His Val Ala Gly Cys Gly Ile Thr Asp Glu Val Ser Gln Trp
187 275 280 285
188 Met Glu Asn Ile Gln Asn Ser Ala Val Glu Glu Leu Pro Glu Pro Met
189 290 295 300
190 Ser Lys Asp Tyr Gln Lys Leu His Arg Lys Gln Leu His Lys Lys Ser
191 305 310 315 320
192 Ala Pro Gln Gln Gln Gln Pro His Pro Pro Lys Lys Tyr Ile Ser
193 325 330 335
194 Gly Asp Glu Asp Phe Lys Tyr Pro His Gln Lys Tyr Thr Lys Glu Ala
195 340 345 350
196 Asn Phe Ala Glu Gly Ala Phe Tyr Asp Pro Ser Thr Gly Arg Arg Leu
197 355 360 365
198 Gly Ser Ser Ala Asn Val Ala Asp Trp His Gln Leu Val His Glu Arg
199 370 375 380
200 Val Arg Arg Ala Thr Asp Asn Gly Ala Gly Asp Arg Gly Ser Ser Gly

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201	385				390					395				400
202	Gly	Ser	Gly	Arg	Gly	Arg	Glu	Asp	Asn	Lys	Asn	Thr	Cys	Ser
203					405					410				415
204	Ile	Gln	Thr	Asp	Pro	Leu	Ile	Trp	Arg	His	Ile	Arg	Glu	Gly
205				420					425					430
206	Asp	His	Asp	Arg	Gly	Arg	Lys	Tyr	Glu	Val	Asp	Glu	Lys	Thr
207			435					440					445	
208	Glu	Ile	Thr	Ser	Leu	Ile	Ala	His	His	Val	Thr	Ala	Val	Asn
209		450					455					460		
210	Tyr	Arg	Asn	Thr	Lys	Phe	Asp	Gly	Arg	Thr	Glu	His	Arg	Asn
211	465					470					475			480
212	Phe	Glu	Val	Gln	Arg	Ile	Lys	Ile	Asp	Asp	Ser	Ala	Cys	Arg
213				485					490					495
214	Ser	Tyr	Asn	Gly	Pro	His	Asn	Ala	Phe	Cys	Asn	Glu	His	Met
215			500						505					510
216	Ser	Asn	Phe	Leu	Asn	Leu	His	Ser	Leu	Glu	Asp	His	Ser	Asp
217		515						520					525	
218	Leu	Ala	Tyr	Val	Phe	Thr	Tyr	Arg	Asp	Phe	Thr	Gly	Gly	Thr
219		530					535					540		
220	Leu	Ala	Trp	Val	Ala	Ser	Ala	Ser	Gly	Ala	Ser	Gly	Gly	Ile
221	545					550				555				560
222	Lys	Tyr	Lys	Thr	Tyr	Thr	Glu	Thr	Val	Gly	Gly	Gln	Tyr	Gln
223				565					570					575
224	Lys	Arg	Ser	Leu	Asn	Thr	Gly	Ile	Ile	Thr	Phe	Val	Asn	Tyr
225			580					585						590
226	Arg	Val	Pro	Pro	Lys	Val	Ser	Gln	Leu	Thr	Leu	Ala	His	Glu
227		595					600						605	
228	His	Asn	Phe	Gly	Ser	Pro	His	Asp	Tyr	Pro	Gln	Glu	Cys	Arg
229		610					615					620		
230	Gly	Leu	Asn	Gly	Asn	Tyr	Ile	Met	Phe	Ala	Ser	Ala	Thr	Ser
231	625				630					635				640
232	Arg	Pro	Asn	Asn	Ser	Lys	Phe	Ser	Pro	Cys	Ser	Ile	Arg	Asn
233				645					650					655
234	Asn	Val	Leu	Asp	Val	Leu	Val	Gly	Asn	Thr	Lys	Arg	Asp	Cys
235			660					665					670	
236	Ala	Ser	Glu	Gly	Ala	Phe	Cys	Gly	Asn	Lys	Ile	Val	Glu	Ser
237		675					680					685		
238	Glu	Cys	Asp	Cys	Gly	Phe	Asn	Glu	Glu	Glu	Cys	Lys	Asp	Lys
239		690				695					700			
240	Tyr	Pro	Arg	Leu	Ile	Ser	Glu	Tyr	Asp	Gln	Ser	Leu	Asn	Ser
241	705				710					715				720
242	Lys	Gly	Cys	Thr	Arg	Arg	Ala	Lys	Thr	Gln	Cys	Ser	Pro	Ser
243				725					730					735
244	Pro	Cys	Cys	Leu	Ser	Asn	Ser	Cys	Thr	Phe	Val	Pro	Thr	Ser
245			740					745					750	
246	Gln	Lys	Cys	Lys	Glu	Glu	Thr	Glu	Cys	Ser	Trp	Ser	Ser	Thr
247		755					760					765		
248	Gly	Thr	Thr	Ala	Glu	Cys	Pro	Glu	Pro	Arg	His	Arg	Asp	Asp
249		770				775						780		

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L:25 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:26 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]